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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/500,646	10/12/2004	Claude Mabilat	120162	2871

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EXAMINER	
MYERS, CARLA J	
ART UNIT	**PAPER NUMBER**
1634	

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Please find below and/or attached an Office communication concerning this application or proceeding.

The time period for reply, if any, is set in the attached communication.

Office Action Summary	Application No.	Applicant(s)	
	10/500,646	MABILAT ET AL.	
	Examiner	Art Unit	
	Carla Myers	1634	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *13 June 2007*.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-17* is/are pending in the application.

4a) Of the above claim(s) *3, 5-8 and 10-17* is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *1,2,4 and 9* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO/SB/08) Paper No(s)/Mail Date *3/4/2005*.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____ .
5) ☐ Notice of Informal Patent Application
6) ☐ Other: _____.

DETAILED ACTION

Election/Restrictions

1. Applicant's election with traverse of Group I and the combination of sequences of SEQ ID NO: 1-232 and 242-261 in the reply filed on June 13, 2007 is acknowledged. The traversal is on the ground(s) that the technical feature linking the claimed invention is the combination of sequences of SEQ ID NO: 1-232 and 242-261. It is argued that a search of the remaining claims would not require undue burden. This is not found persuasive because restriction is proper in a 371 application if there is no special technical feature linking the claimed inventions. In the present situation, the claims of groups II, III and IV are not limited to the technical feature of the combination of each of SEQ ID NO: 1-232 and 242-261. Rather, the claims of groups III and IV are directed to nucleic acids and methods, respectively, which require the nucleic acids of SEQ ID NO: 262-271. Further, the claims of group II are not limited to the entire combination of each of SEQ ID NO: 1-232 and 242-261. Moreover, the claims of group II read on any combination of 10 mers and thereby are anticipated by the teachings of Fodor (PGPUB 2001/0053519) wherein arrays are disclosed comprising all possible combinations of 10mers. Thereby, there is no special technical feature linking the claimed inventions, as would be required to show unity of invention.

The requirement is still deemed proper and is therefore made FINAL.

2. Claims 1, 2, 4 and 9 have been examined herein only to the extent that the claims read on the elected invention of the specific combination of each of the nucleic acids of SEQ ID NO: 1-232 and 242-261. The non-elected subject matter methods which require

the use of the individual nucleic acids or other combinations of nucleic acids is withdrawn from consideration as being drawn to a non-elected invention. Additionally, claims 3, 5-8 and 10-17 are withdrawn from consideration as being drawn to a non-elected invention.

Claim Objections

3. Claims 1, 2, 4 and 9 are objected to because the claims include subject matter of the non-elected inventions, namely the individual nucleic acids and additional combination of nucleic acids selected from the group consisting of SEQ ID NO: 1-232 and 242-261.

4. Claim 4 is objected to because the claim depends from a non-elected claim.

Claim Rejections - 35 USC § 112 second paragraph

5. The following is a quotation of the second paragraph of 35 U.S.C. 112:

> The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

Claims 1, 2, 4 and 9 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

Regarding claims 1, 2, 4 and 9, the phrase "for example fragment" (claim 1, step b) renders the claim indefinite because it is unclear whether the limitation(s) following the phrase are part of the claimed invention. See MPEP § 2173.05(d).

Claims 1, 2 and 9 are indefinite because the claims do not recite a clear nexus between the preamble of the claims and the final step of the claims. The claims are drawn to methods for determining an original animal species. However, the final step is one in which a signal or item of information is determined. Accordingly, it is unclear as

to whether the claims are intended to be limited to general methods for detecting a signal or item of information or to methods for determining an original animal species. In the later case, the claims do not set forth how the determining a signal or item of information results in the determination of an original animal species.

Claims 1, 2 and 9 are indefinite because the claims do not recite the basic steps of the claimed method in a positive, active fashion. See Ex parte Erlich 3 USPQ2d, 1011 (BPAI 1986). The claims are written in the passive tense of, for example, "is provided" and "are brought into contact," whereas the claims should recite the active tense of "providing" and "contacting."

Claims 1, 2 and 9 are also indefinite over the recitation of "any signal or item of information resulting from the specific reaction between said reagent and the nucleic acid fraction, characterizing the presence in said sample of said original animal species, is determined by means of detection" because it is unclear as what is intended to be meant by this phrase. The phrase "the specific reaction" lacks proper antecedent basis since the claims do not previously recite a step in which a specific reaction occurs. Rather, the claims recite only a step of contacting a nucleic acid fraction and a reagent. Also, the claims do not recite a step of generating a signal or an item of information and thereby it is unclear as to what constitutes the signal or item of information to be detected. Accordingly, it is unclear as to what is intended to be encompassed by the detection of the signal or item of information that results from the specific reaction between the nucleic acid fraction and the reagent.

Claims 1, 2, 4 and 9 are indefinite over the recitation of "the complementarity meaning any sequence capable of hybridizing." Capability is a latent characteristic and the claims do not set forth the criteria by which to determine capability. That is, it is not clear whether the recited sequences do in fact hybridize or only have the potential to hybridize under some unspecified conditions or following some unstated modification of the sequences. Amendment of the claim to read e.g. "...which hybridizes" would obviate this rejection.

Claim 2 is indefinite over the recitation of "said reagents specific for the same original species and/or respectively different original animal species" because this phrase lacks proper antecedent basis. While the claim previously refers to "at least one reagent specific for the animal species" the claim does not previously refer to "reagents specific for the same original species and/or respectively different original animal species."

Claim 9 is indefinite because it is unclear as to what is intended to be the relationship between the biochip of claim 9 and the reagents of claim 2. For example, it is unclear as to whether the biochip used in the determining step of claim 9 is used in addition to or in place of the reagents of claim 2, or whether claim 9 is intended to further define the reagents of claim 2 such that the reagents of claim 2 are attached to a biochip.

Claim 9 is indefinite over the recitation of "a developed surface." This phrase is not defined in the specification and it is unclear as to what constitutes such a developed surface.

Claim 4 provides for the use of nucleotide sequences, but, since the claim does not set forth any steps involved in the method/process, it is unclear what method/process applicant is intending to encompass. A claim is indefinite where it merely recites a use without any active, positive steps delimiting how this use is actually practiced.

Claim Rejections - 35 USC § 101

6. Claim 4 is rejected under 35 U.S.C. 101 because the claimed recitation of a use, without setting forth any steps involved in the process, results in an improper definition of a process, i.e., results in a claim which is not a proper process claim under 35 U.S.C. 101. See for example *Ex parte Dunki*, 153 USPQ 678 (Bd.App. 1967) and *Clinical Products, Ltd.* v. *Brenner*, 255 F. Supp. 131, 149 USPQ 475 (D.D.C. 1966).

Claim Rejections - 35 USC § 112 – Written Description

7. The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

Claims 1, 2, 4 and 9 are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention. This is a Written Description rejection.

In analyzing claims for compliance with the written description requirement of 35 U.S.C. 112, first paragraph, the written description guidelines note that with regard to

genus/species situations, a "Satisfactory disclosure of a "representative number" depends on whether one of skill in the art would recognize that the applicant was in possession of the necessary common attributes or features of the elements possessed by the members of the genus in view of the species disclosed." (See: Federal Register: December 21, 1999 (Volume 64, Number 244), revised guidelines for written description.)

To provide adequate written description and evidence of possession of a claimed genus, the specification must provide sufficient distinguishing identifying characteristics of the genus. The factors to be considered include disclosure of a complete or partial structure, physical and/or chemical properties, functional characteristics, structure/function correlation, and any combination thereof.

Thereby, to ascertain whether the written description requirement is met for a genus claim, it is first determined whether a representative number of species have been described by their complete structure. It is then determined whether a representative number of species have been defined by other identifying characteristics.

In the present situation, the claims are drawn to methods of determining an original animal species in a sample comprising contact a nucleic acid fraction from said sample with at least one reagent specific for an animal species and detecting a signal or "item of information" from the reaction between the reagent and the nucleic acid fraction, wherein the at least one reagent consists of i) each of the sequences of SEQ ID NO: 1-232 and 242-261 or ii) sequences sharing complementarity with SEQ ID NO: 1-232 and 242-261, wherein the sequences "are capable of hybridizing" at between 20

to 70°C in a saline solution of 0.5M to 1M to the sequences of SEQ ID NO: 1-232 and 242-261; or iii) sequences that share any level of homology to SEQ ID NO: 1-232 and 242-261 or sequences having any level of complementarity to the sequences of SEQ ID NO: 1-232 and 242-261 and wherein "homology" includes but is not limited to sequences that comprise 5 contiguous nucleotides of the recited sequences and have 70% with said sequences. Accordingly, as broadly written, the claims include a significantly large genus of reagents.

In particular, the phrase "specific for the animal species" has not been clearly defined in the specification and this phrase has many distinct meanings in the art. For example, it is unclear as to whether such nucleic acids hybridize only to only one animal species under all hybridization conditions or under only particular unspecified hybridization conditions or whether the nucleic acids may hybridize to additional animal species under other unspecified hybridization conditions.

Absent a specific definition in the specification, the language "specific for" has been interpreted broadly and is not considered to impart any particular structural or functional limitations onto the nucleic acid reagents.

Regarding ii) above, the claims define the nucleic acids in terms of the fact that they are capable of hybridizing under the stated hybridization conditions. The phrase "capable of hybridizing" is not defined in the specification and therefore has been given its broadest reasonable interpretation as including nucleic acids which may or may not hybridize to SEQ ID NO: 1-232 and 242-261. Further, the recited conditions are very broad and include low stringency hybridization conditions. As such the claims read on

nucleic acids which comprise sequences sharing low levels, such as 40% etc, with SEQ ID NO: 1-232 and 242-261 and fragments thereof.

Regarding iii) above, the claims define only 5 nucleotides of the recited sequences and it appears that the 5 nucleotides may have as little as 70% identity with 5 nucleotides of SEQ ID NO: 1-232 and 242-261. The nucleotides flanking the 5 nucleotides are not defined in terms of their nucleotide sequence or length.

Accordingly, the claims encompass methods which require the use of a phenomenally large genus of reagents for an animal species.

However, the specification discloses a limited number of nucleic acids and does not describe the functional properties of these nucleic acids. In particular, the specification discloses the nucleic acids consisting of SEQ ID NO: 1-232 and 242-261. The specification does not characterize the hybridization specificity of these nucleic acids. The sequence listing identifies the species from which the nucleic acids were derived. For example, SEQ ID NO: 1 was obtained from Anas platyrhynchos. However, the specification does not teach if SEQ ID NO: 1 hybridizes only to A. platyrhynchos (and under what conditions) and distinguishes this species from other Anas species or if SEQ ID NO: 1 also cross hybridizes with other Anas species or other non-Anas species. Given the limited information provided in the specification, it cannot be ascertained as to whether the specification teaches any particular nucleic acids consisting of a sequence that hybridizes specifically to one animal species and distinguishes that one animal species from other animal species.

For example, SEQ ID NO: 9 is characterized in the sequence listing as being obtained from Cairina moschata (Muscovy duck). However, the sequence of SEQ ID NO: 9 is also present in, and therefore will cross-hybridize to and detect, Siganus rivulatus (rabbitfish; GenBank Accession No. AY24940):

```
Qy          1 AACCTGCACGCCAATG 16
              ||||||||||||||||
Db        110 AACCTGCACGCCAATG 95
```

SEQ ID NO: 9 is also present in, and therefore will cross-hybridize to and detect, Gerrhosaurus flavigularis (lizard; GenBank Accession No. AY17383):

```
Qy          1 AACCTGCACGCCAATG 16
              ||||||||||||||||
Db        229 AACCTGCACGCCAATG 244
```

Similarly, while SEQ ID NO: 8 is characterized as being obtained from Anser anser, this sequence is also present in, and therefore will cross-hybridize to and detect, Anser albifrons (GenBank Accession No. AY072598):

```
Qy          1 CACTTCACTCGCCTTCTC 18
              ||||||||||||||||||
Db         77 CACTTCACTCGCCTTCTC 94
```

SEQ ID NO: 8 also shares 94% identity with, and therefore will cross-hybridize to and detect, Enterobacter cloacae (GenBank Accession No. AEH54479):

```
Qy          1 CACTTCACTCGCCTTCTC 18
              || ||||||||||||||||
Db        636 CAATTCACTCGCCTTCTC 619
```

Further, nucleotides 1-17 of SEQ ID NO: 8 are present in and therefore will cross-hybridize to and detect, Mus musculus(GenBank Accession No. BB278453):

```
Qy          1 CACTTCACTCGCCTTCT 17
              |||||||||||||||||
Db         57 CACTTCACTCGCCTTCT 73
```

The specification also teaches the primers of SEQ ID NO: 240 and 241 which are universal primers that amplify all animal species. The specification further teaches a number of "signature sequence" consisting of SEQ ID NO: 23-239 and 262-271. However, the present claims are not directed to these sequences, but rather are directed to variants of SEQ ID NO: 1-232 and 242-261. Further, the recited sequences do not appear to be specific for only a single animal species, but rather also hybridize with other species within the same or a different genus. For example, the specification (page 50) discloses the sequence of SEQ ID NO: 262 and indicates that this sequence was obtained from Bos Taurus and hybridizes to sequences within mammals. For instance, the sequence of SEQ ID NO: 262 is identical to a sequence present in Silka deer (GenBank Accession No. AY245522):

```
Qy          1 CTAATCCTACAAATC 15
              |||||||||||||||
Db          4 CTAATCCTACAAATC 18
```

and Puma (GenBank Accession No. AF499775):

```
Qy          1 CTAATCCTACAAATC 15
              |||||||||||||||
Db         26 CTAATCCTACAAATC 40
```

Accordingly, the specification describes nucleic acids consisting of SEQ ID NO: 1-232 and 242-261 in terms of their complete structure, but does not characterize these nucleic acids as "specific for" any particular animal species.

No additional members of the claimed genus have been sufficiently described in terms of any other relevant identifying characteristics (e.g. restriction map, biological activity of an encoded protein product, etc.).

In the absence of a representative number of species of the claimed genus, there is insufficient descriptive support for the currently claimed genus of reagents that are specific for an animal species and which share minimal complementarity with SEQ ID NO: 1-232 and 242-261 or which comprise any 5 nucleotides or 5 nucleotides having 70% identity with SEQ ID NO: 1-232 and 242-261 or sequences having any level (1% etc), with SEQ ID NO: 1-232 and 242-261, flanked by nucleotides of any identity and length.

The decisional law in this area has been very consistent. The Federal Circuit in Lilly, Fiers, Rochester and many other cases has determined that the written description issue applies to situations where the definition of the subject matter of the claims fails to provide description commensurate with the genus. The most recent case law directly supports this rejection. As the District Court in University of Rochester v. G.D. Searle & Co., Inc. (2003 WL 759719 W.D.N.Y.,2003. March 5, 2003.) noted "In effect, then, the '850 patent claims a method that cannot be practiced until one discovers a compound that was not in the possession of, or known to, the inventors themselves. Putting the claimed method into practice awaited someone actually discovering a necessary component of the invention." This is similar to the current situation since the breadth of the current claims comprises the use of millions of possible different reagents which the

present inventors were not in the possession of, or which were not known to the inventors.

As noted in Vas-Cath Inc. v. Mahurkar (19 USPQ2d 1111, CAFC 1991), the Federal Circuit concluded that:

"...applicant must also convey, with reasonable clarity to those skilled in art, that applicant, as of filing date sought, was in possession of invention, with invention being, for purposes of "written description" inquiry, whatever is presently claimed."

Applicant is reminded that *Vas-Cath* makes clear that the written description provision of 35 U.S.C. 112 is severable from its enablement provision.

With respect to the present invention, there is no record or description which would demonstrate conception of the broadly claimed genus of reagents specific for an animal species. Therefore, the claims fail to meet the written description requirement because the claims encompass a significantly large genus of polynucleotide sequences which are not described in the specification.

Claim Rejections - 35 USC § 112 - Enablement

8. Claims 1, 2, 4 and 9 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the enablement requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to enable one skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention.

The following factors have been considered in formulating this rejection (*In re Wands,* 858F.2d 731, 8 USPQ2d 1400 (Fed. Cir. 1988): the breadth of the claims, the nature of the invention, the state of the prior art, the relative skill of those in the art, the

predictability or unpredictability of the art, the amount of direction or guidance presented, the presence or absence of working examples of the invention and the quantity of experimentation necessary.

Breadth of the Claims:

The claims are drawn to methods of determining an original animal species in a sample comprising contact a nucleic acid fraction from said sample with at least one reagent specific for an animal species and detecting a signal or "item of information" from the reaction between the reagent and the nucleic acid fraction, wherein the at least one reagent consists of i) each of the sequences of SEQ ID NO: 1-232 and 242-261 or ii) sequences sharing complementarity with SEQ ID NO: 1-232 and 242-261, wherein the sequences "are capable of hybridizing" at between 20 to 70°C in a saline solution of 0.5M to 1M to the sequences of SEQ ID NO: 1-232 and 242-261; or iii) sequences that share any level of homology to SEQ ID NO: 1-232 and 242-261 or sequences having any level of complementarity to the sequences of SEQ ID NO: 1-232 and 242-261 and wherein "homology" includes but is not limited to sequences that comprise 5 contiguous nucleotides of the recited sequences and have 70% with said sequences. Accordingly, as broadly written, the claims include a significantly large genus of reagents.

In particular, the phrase "specific for the animal species" has not been clearly defined in the specification and this phrase has many distinct meanings in the art. For example, it is unclear as to whether such nucleic acids hybridize only to only one animal species under all hybridization conditions or under only particular unspecified hybridization conditions or whether the nucleic acids may hybridize to additional animal

species under other unspecified hybridization conditions. Absent a specific definition in the specification, the language "specific for" has been interpreted broadly and is not considered to impart any particular structural or functional limitations onto the nucleic acid reagents.

Regarding ii) above, the claims define the nucleic acids in terms of the fact that they are capable of hybridizing under the stated hybridization conditions. The phrase "capable of hybridizing" is not defined in the specification and therefore has been given its broadest reasonable interpretation as including nucleic acids which may or may not hybridize to SEQ ID NO: 1-232 and 242-261. Further, the recited conditions are very broad and include low stringency hybridization conditions. As such the claims read on nucleic acids which comprise sequences sharing low levels, such as 40% etc, with SEQ ID NO: 1-232 and 242-261 and fragments thereof.

Regarding iii) above, the claims define only 5 nucleotides of the recited sequences and it appears that the 5 nucleotides may have as little as 70% identity with 5 nucleotides of SEQ ID NO: 1-232 and 242-261. The nucleotides flanking the 5 nucleotides are not defined in terms of their nucleotide sequence or length.

Accordingly, the claims encompass methods which require the use of a phenomenally large genus of reagents for the detection of original animal species, wherein the nucleic acid sequences are not defined in terms of their complete chemical structure or in terms of their specific functional properties (i.e., the particular organisms to which the nucleic acid sequences hybridize under a certain set of hybridization conditions).

Nature of the Invention:

The claims are drawn to methods of detecting an original animal species comprising contacting a nucleic acid sample with a nucleic acid reagent. The invention is in a class of invention which the CAFC has characterized as "the unpredictable arts such as chemistry and biology." Mycogen Plant Sci., Inc. v. Monsanto Co., 243 F. 3d 1316, 1330 (Fed Cir. 2001).

Teachings in the Specification and State of the Art:

The specification discloses the nucleic acids consisting of SEQ ID NO: 1-232 and 242-261. The sequence listing identifies the species from which the nucleic acids were derived. However, the specification itself does not provide any information regarding the specificity of the nucleic acids. No data is provided, for instance, showing that any particular probe hybridizes to one or more "original animal species." No information is provided as to the hybridization conditions that would be required to use the sequences of SEQ ID NO: 1-232 and 242-261 to detect specific animal species. For example, SEQ ID NO: 1 was obtained from Anas platyrhynchos. However, the specification does not teach if SEQ ID NO: 1 hybridizes only to A. platyrhynchos (and under what conditions) and distinguishes this species from other Anas species or if SEQ ID NO: 1 also cross hybridizes with other Anas species or other non-Anas species.

Given the limited information provided in the specification, it cannot be ascertained as to whether the specification teaches any particular nucleic acids consisting of a sequence that hybridizes specifically to one animal species and which distinguishes that one animal species from other animal species.

For example, SEQ ID NO: 9 is characterized in the sequence listing as being obtained from Cairina moschata (Muscovy duck). However, the sequence of SEQ ID NO: 9 is also present in, and therefore will cross-hybridize to and detect, Siganus rivulatus (rabbitfish; GenBank Accession No. AY24940):

```
Qy          1 AACCTGCACGCCAATG 16
              ||||||||||||||||
Db        110 AACCTGCACGCCAATG 95
```

SEQ ID NO: 9 is also present in, and therefore will cross-hybridize to and detect, Gerrhosaurus flavigularis (lizard; GenBank Accession No. AY17383):

```
Qy          1 AACCTGCACGCCAATG 16
              ||||||||||||||||
Db        229 AACCTGCACGCCAATG 244
```

Similarly, while SEQ ID NO: 8 is characterized as being obtained from Anser anser, this sequence is also present in, and therefore will cross-hybridize to and detect, Anser albifrons (GenBank Accession No. AY072598):

```
Qy          1 CACTTCACTCGCCTTCTC 18
              ||||||||||||||||||
Db         77 CACTTCACTCGCCTTCTC 94
```

SEQ ID NO: 8 also shares 94% identity with, and therefore will cross-hybridize to and detect, Enterobacter cloacae (GenBank Accession No. AEH54479):

```
Qy          1 CACTTCACTCGCCTTCTC 18
              || ||||||||||||||||
Db        636 CAATTCACTCGCCTTCTC 619
```

Further, nucleotides 1-17 of SEQ ID NO: 8 are present in, and therefore will cross-hybridize to and detect, Mus musculus (GenBank Accession No. BB278453):

```
Qy          1 CACTTCACTCGCCTTCT 17
              |||||||||||||||||
Db         57 CACTTCACTCGCCTTCT 73
```

Regarding SEQ ID NO: 4, this nucleic acid shares 91.7% identity with, and therefore will cross hybridize with Pimephales promelas (GenBank Accession No. DT268277):

```
Qy          1 GACACATCCCTTGCTTTCTCCTCA 24
              |||||||||||||  |||||||  ||
Db        422 GACACATCCCTTGGTTTCTCCCCA 399
```

Regarding SEQ ID NO: 3, this nucleic acid shares 88% identity with, and therefore will cross hybridize with Oryzias latipes (Japanese killfish; GenBank Accession No. DE063816):

```
Qy          7 TCTCTGCTCGCCATCTGCCTGGCCACACAAAT 38
              |||||||||  ||||||||  ||   |||||||||
Db        188 TCTCTGCTCTCCATCTGCTTGAACACACAAAT 219
```

Regarding SEQ ID NO: 2, nucleotides 1-18 are 100% identical to sequences in the Schistosoma mansoni genome and therefore this sequence and 5mer fragments thereof will hybridize to Schistosoma mansoni DNA (GenBank Accession No. DX987659):

```
Qy          1 GTAATCCTACTGCTCACT 18
              ||||||||||||||||||
Db         48 GTAATCCTACTGCTCACT 31
```

Regarding SEQ ID NO: 1, this sequence shares 94% identity to sequences in the human genome and therefore this sequence and 5mer fragments thereof will hybridize to human DNA (GenBank Accession No. ADR07925):

```
Qy          1 CTCCTACTGGCTATGCAC 18
              ||||| ||||||||||||
Db       1592 CTCCTGCTGGCTATGCAC 1609
```

Additionally, the sequence of SEQ ID NO: 1 is identical to sequences present in Aedes aegypti (yellow fever mosquito; GenBank Accession No: DV296868). Therefore, SEQ ID NO: 1 will cross-hybridize with and detect nucleic acids present in a sample that are from Aedes aegypti:

```
Qy          1 CTCCTACTGGCTATGCAC 18
              ||||||||||||||||||
Db         81 CTCCTACTGGCTATGCAC 98
```

The specification also teaches the primers of SEQ ID NO: 240 and 241 which are universal primers that amplify all animal species. The specification further teaches a number of "signature sequence" consisting of SEQ ID NO: 23-239 and 262-271. However, the present claims are not directed to these sequences, but rather are directed to variants of SEQ ID NO: 1-232 and 242-261. Further, the recited sequences do not appear to be specific for only a single animal species, but rather also hybridize with other species within the same or a different genus. For example, the specification (page 50) discloses the sequence of SEQ ID NO: 262 and indicates that this sequence was obtained from Bos Taurus and hybridizes to sequences within mammals. For instance, the sequence of SEQ ID NO: 262 is identical to a sequence present in Silka deer (GenBank Accession No. AY245522):

```
Qy          1 CTAATCCTACAAATC 15
              |||||||||||||||
Db          4 CTAATCCTACAAATC 18
```

and Puma (GenBank Accession No. AF499775):

```
Qy          1 CTAATCCTACAAATC 15
              ||||||||||||||
Db         26 CTAATCCTACAAATC 40
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The Predictability or Unpredictability of the Art and Degree of Experimentation:

The prior art acknowledges the unpredictability in modifying the nucleotide sequence of a gene. Modification of even a single nucleotide within a nucleic acid sequence can significantly alter the specificity of hybridization of that sequence. This finding is evidenced by the teachings above wherein the change at nucleotide position within SEQ ID NO: 8 results in a probe that cross-hybridizes with Enterococcus cloacae and wherein the deletion of a terminal nucleotide results in a probe that cross-hybridizes with Mus musculus. The specification does not provide any information as to regions of SEQ ID NO: 1-232 and 242-261 which are critical for functional activity and for maintaining the hybridization specificity of the probe. It is unpredictable as to which nucleotides can be inserted or deleted or substituted within SEQ ID NO: 1-232 and 242-261 without altering the specificity of the probe. It is also unpredictable as how adding nucleotides of any identity or length to SEQ ID NO: 1-232 and 242-261 or 5mer fragments thereof will effect the functional properties of the resulting nucleic acids. Most importantly, it remains highly unpredictable as to how the combination of nucleic acids of SEQ ID NO: 1-232 and 242-261 can be used to determine an original animal species since these nucleic acids appear to cross-hybridize with other species and the specificity of hybridization of these nucleic acids has not been disclosed in the specification

Amount of Direction or Guidance Provided by the Specification:

The specification does not provide any specific guidance as to how to predictably make and use the nucleic acids of SEQ ID NO: 1-232 and 242-261 to detect an original animal species. As discussed above, the sequence listing identifies the source of the nucleic acids, yet, the specification does not teach which animal species the probes hybridize to and the conditions under which such hybridization occurs. The specification also fails to provide sufficient guidance as to how to make and use variants of the nucleic acids to determine an original animal species. Again, modification of the nucleic acids by the substitution, addition or deletion of even 1 nucleotide significantly alters the specificity of hybridization of the nucleic acids. No guidance is provided in the specification as to which nucleotides within SEQ ID NO: 1-232 and 242-261 can be added, deleted or substituted and what will be the result of such modifications. Also, no guidance is provided as to what nucleotides and the number of the nucleotides that can be added to the terminus of SEQ ID NO: 1-232 and 242-261 and 5mer fragments thereof and no guidance is provided as to how to use the resulting nucleic acids to detect particular animal species.

While the artisan could generate a significantly large genus of nucleic acids in which nucleotides of any identity are added to the 5' or 3' terminus of SEQ ID NO: 1-232 and 242-261 and 5mer fragments thereof or in which any number of nucleotides within SEQ ID NO: 1-232 and 242-261 are mutated via substitution, addition or deletion, and then assay each of these nucleic acids to try to determine their specificity of hybridization under particular conditions of hybridization, such trial-by-error experimentation is considered to be undue. Providing methods for searching for

additional nucleic acids and trying to determine the function of the resulting nucleic acid is not equivalent to teaching how to make and use specific nucleic acids.

Working Examples:

Again, the specification teaches only the nucleic acid of SEQ ID NO: 1-232 and 242-261 and the Sequence Listing recites the source of these nucleic acids. However, the specification does not provide any examples of using these nucleic acids to detect one or more specific animal species. Further, the specification does not exemplify a representative number of variants of SEQ ID NO: 1-232 and 242-261 and methods of using said variants to detect original animal species, wherein the variants may share minimal (e.g., 30% or 40%) identity with SEQ ID NO: 1-232 and 242-261 or may share 70% identity with 5 nucleotides of SEQ ID NO: 1-232 and 242-261 or any sequence having any level of sequence complementarity thereto and may further include nucleotides of any identity and length.

Conclusions:

Case law has established that "(t)o be enabling, the specification of a patent must teach those skilled in the art how to make and use the full scope of the claimed invention without 'undue experimentation.'" *In re Wright* 990 F.2d 1557, 1561. *In re Fisher,* 427 F.2d 833, 839, 166 USPQ 18, 24 (CCPA 1970) it was determined that "(t)he scope of the claims must bear a reasonable correlation to the scope of enablement provided by the specification to persons of ordinary skill in the art". The amount of guidance needed to enable the invention is related to the amount of knowledge in the art as well as the predictability in the art. Furthermore, the Court in *Genetech Inc. v*

Novo Nordisk 42 USPQ2d 1001 held that "(I)t is the specification, not the knowledge of one skilled in the art that must supply the novel aspects of the invention in order to constitute adequate enablement". In the instant case, the specification does not disclose the specificity of any of the hybridization probes consisting of SEQ ID NO: 1-232 and 242-261 and does not provide sufficient guidance to enable the skilled artisan to use these probes to detect specific animal species and to distinguish between particular animal species. Further, the claims do not bear a reasonable correlation to the scope of enablement because while the specification teaches nucleic acids consisting of SEQ ID NO: 1-232 and 242-261, the claims broadly encompass millions upon millions of possible variants of these nucleic acids, in which the overall structural and functional properties of the nucleic acids are not defined. Accordingly, although the level of skill in the art of molecular biology is high, given the lack of disclosure in the specification and in the prior art, it would require undue experimentation for one of skill in the art to make and use the broadly claimed invention.

Claim Rejections - 35 USC § 102

9. The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

> A person shall be entitled to a patent unless –
>
> (b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

Claims 1, 2, 4 and 9 are rejected under 35 U.S.C. 102(b) as being anticipated by Fodor (2001/0053519).

The present claims have been interpreted as being drawn to a method comprising providing a nucleic acid fraction, providing a reagent, contacting the nucleic acid fraction with the reagent, and detecting any signal generated from the resulting contacting step. As noted in the MPEP 211.02, " a preamble is generally not accorded any patentable weight where it merely recites the purpose of a process or the intended use of a structure, and where the body of the claim does not depend on the preamble for completeness but, instead, the process steps or structural limitations are able to stand alone." Further, in *Pitney Bowes Inc. v. Hewlett-Packard Co.*, 182F.3d 1298, 1305, 51 USPQ2d 1161, 1166 (Fed Cir. 1999) the court held that if the body of the claim sets forth the complete invention, and the preamble is not necessary to give "life, meaning and vitality" to the claim, "then the preamble is of no significance to claim construction because it cannot be said to constitute or explain a claim limitation". In the present situation, the claim language of "for determining an original animal species" is a statement of purpose and intended result and does result in a manipulative difference in the method steps of the claims. Accordingly, the process steps are able to stand alone and therefore the preamble limitation is not accorded patentable weight. Further, the claims have been interpreted as encompassing the use of reagents wherein the reagents comprise any 5 contiguous nucleotides of each of SEQ ID NO: 1-232 and 242-261, or sequences having 70% identity with any 5 contiguous nucleotides of each of SEQ ID NO: 1-232 and 242-261, or sequences comprising any 5 contiguous nucleotides of a sequence that shares any level of sequence complementarity with SEQ ID NO: 1-232 and 242-261. Lastly, the phrase "specific for the animal species" has

not been clearly defined in the specification. Absent a specific definition for this phrase, the language "specific for" has been interpreted broadly and is not considered to impart any particular structural or functional limitations onto the nucleic acid reagents.

Fodor teaches methods comprising obtaining a nucleic acid fraction from a sample, providing a set of reagents attached to an array, each reagent comprising a nucleic acid sequence, contacting the nucleic acid sequence with the set of reagents, and detecting a signal that is generated as a result of the reaction between the set of reagents and the nucleic acid fraction (see, e.g., para [0083]). In the method of Fodor, the nucleic acid fraction is obtained from animals, and thereby the nucleic acid fraction is obtained from a sample that is liable to obtained an "ingredient" (e.g., cellular material, nucleic acids, proteins) obtained from at least one animal species (para [0088] and [0093]). Further, Fodor (para [0122], Figures 2-5) teaches that the nucleic acid arrays comprise all possible 10 mers. Accordingly, the set of nucleic acids comprising all possible 10 mers meet the limitations of the claims of, for example, nucleic acids comprising 5 nucleotides of SEQ ID NO: 1-232 and 242-261, or sequences complementary thereto or having 70% identity thereto.

Regarding claim 2, in the method of Fodor (Example 2), a set of probes (i.e., a multiplicity of reagents) is used and a multiplicity of signals are generated and detected as indicative of the target nucleic acid to be detected.

Regarding claim 4, this claim does not recite any active process steps. Thereby, the method of Fodor anticipates the claimed method.

Regarding claim 9, Fodor teaches that the nucleic acid reagents are immobilized onto a solid support that has a surface to which the probes are arranged and attached in a predetermined arrangement (see, e.g., paras [0073], [0081] and [0083]).

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Carla Myers whose telephone number is 571-272-0747. The examiner can normally be reached on Monday-Thursday (6:30-5:00).

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Ram Shukla can be reached on 571-272-0782. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free). If you would like assistance from a USPTO Customer Service Representative or access to the automated information system, call 800-786-9199 (IN USA OR CANADA) or 571-272-1000.

/Carla Myers/
Primary Examiner, Art Unit 1634